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OM protein - protein search, using sw model

Run on: December 17, 2003, 15:40:19 ; Search time 21 Seconds
(without alignments)
566.160 Million cell updates/sec

Title: US-09-991-209-2
Perfect score: 1492
Sequence: 1 MKQFSAKHLVAVVTAGHAL.....QGVNNAHTTYFGMTSGACTW 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1492	100.0	281	4	US-08-952-445-28 Sequence 28, Appl
2	1026	68.8	197	4	US-08-952-445-26 Sequence 26, Appl
3	403	27.0	77	3	US-08-975-600-7 Sequence 7, Appl
4	362	24.3	289	4	US-09-007-288E-145 Sequence 145, Appl
5	353.5	23.7	291	1	US-08-434-255-13 Sequence 13, Appl
6	353.5	23.7	291	1	US-08-459-967-13 Sequence 13, Appl
7	353.5	23.7	291	1	US-08-460-327-13 Sequence 13, Appl
8	353.5	23.7	291	1	US-08-459-871-13 Sequence 13, Appl
9	353.5	23.7	291	1	US-08-244-686-4 Sequence 4, Appl
10	353.5	23.7	291	2	US-08-784-651-16 Sequence 16, Appl
11	353.5	23.7	291	2	US-08-921-426-10 Sequence 10, Appl
12	353.5	23.7	291	2	US-08-479-275D-2 Sequence 2, Appl
13	353.5	23.7	291	2	US-08-488-271B-2 Sequence 2, Appl
14	353.5	23.7	291	2	US-08-140-008A-2 Sequence 2, Appl
15	353.5	23.7	291	2	US-08-701-339-2 Sequence 2, Appl
16	353.5	23.7	291	3	US-08-816-915-10 Sequence 10, Appl
17	353.5	23.7	291	3	US-09-024-532-6 Sequence 6, Appl
18	353.5	23.7	291	4	US-09-007-288E-16 Sequence 16, Appl
19	353.5	23.7	291	5	PCT-US95-07743-10 Sequence 10, Appl
20	353.5	23.7	384	4	US-09-295-744A-14 Sequence 14, Appl
21	351.5	23.6	294	4	US-09-007-288E-142 Sequence 142, Appl
22	351.5	23.6	294	4	US-09-007-288E-143 Sequence 143, Appl
23	349	23.4	270	3	US-08-362-525-8 Sequence 8, Appl
24	334	22.4	363	2	US-08-784-651-15 Sequence 15, Appl
25	334	22.4	363	4	US-09-402-664A-11 Sequence 11, Appl
26	328	22.0	269	3	US-09-111-556A-4 Sequence 4, Appl
27	328	22.0	269	3	US-08-360-758-4 Sequence 4, Appl

28	323.5	21.7	297	2	US-08-859-106A-2	Sequence 2, Appl
29	323.5	21.7	297	4	US-09-402-664A-9	Sequence 9, Appl
30	317.5	21.3	297	3	US-09-142-469-2	Sequence 2, Appl
31	307.5	20.6	329	4	US-09-892-074-2	Sequence 2, Appl
32	305	20.4	305	4	US-09-402-664A-12	Sequence 12, Appl
33	305	20.4	349	4	US-09-703-416-2	Sequence 2, Appl
34	305	20.4	349	4	US-09-703-414-2	Sequence 2, Appl
35	301	20.2	350	4	US-09-892-188B-2	Sequence 2, Appl
36	297	19.9	337	2	US-08-784-651-8	Sequence 8, Appl
37	297	19.9	338	2	US-08-784-651-10	Sequence 10, Appl
38	292	19.6	338	2	US-08-784-651-6	Sequence 6, Appl
39	290	19.4	297	3	US-09-111-556A-5	Sequence 5, Appl
40	290	19.4	297	3	US-08-360-758-5	Sequence 5, Appl
41	290	19.4	333	3	US-08-988-111-3	Sequence 3, Appl
42	290	19.4	333	3	US-09-387-922-3	Sequence 3, Appl
43	290	19.4	392	4	US-09-402-664A-10	Sequence 10, Appl
44	290	19.4	392	6	5219753-2	Patent No. 5219753
45	289.5	19.4	336	2	US-08-784-651-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-952-445-28
; Sequence 28, Application US/08952445
; Patent No. 6368833
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: ESTERASE ENZYMES, DNA ENCODING
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International, Inc.
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,445
; FILING DATE: 18-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/722,713
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Stone, Christopher L.
; REGISTRATION NUMBER: 35,696
; REFERENCE/DOCKET NUMBER: GC362-2-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7555
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-952-445-28

Query Match 100.0%; Score 1492; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 4.6e-147; Indels 0; Gaps 0;
Matches 281; Conservative 0; Mismatches 0;
Qy 1 MKQFSAKHLVAVVTAGHALAASTGISEDLYSRVEMATISQAAAYADLCNIPSTIKGE 60
Db 1 MKQFSAKHLVAVVTAGHALAASTGISEDLYSRVEMATISQAAAYADLCNIPSTIKGE 60

Db	61	IIIVFRGTGSDTTLQLDNTVLTLPFDLPQNGCEVHGYYIGWVSVDQVESLVKQQVS	120
Qy	142	QYPDYALTVTGHSGASLAALTAQLSATVDNIRLYTEGPRSCNQAFASYMNDATQASS	201

US-09-007-288E-145
; Sequence 145, Application US/09007288E
; Patent No. 6495357
; GENERAL INFORMATION:
; APPLICANT: Fuglsang, Claus
; APPLICANT: Okkels, Jens
; APPLICANT: Petersen, Dorte

APPLICANT: Patkar, Shankar
APPLICANT: Thellersen, Marianne
APPLICANT: Svenden, Allan
APPLICANT: Borch, Kim
APPLICANT: Royer, John
APPLICANT: Kretschmar, Titus
APPLICANT: Halkier, Torben
APPLICANT: Vind, Jesper
APPLICANT: Jorgensen, Steen
TITLE OF INVENTION: No. 6495357el Lipolytic Enzymes
FILE REFERENCE: 4455.404-US
CURRENT APPLICATION NUMBER: US/09/007.288E
CURRENT FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PatentIn version 3.1
SEQ ID NO 145
LENGTH: 289
TYPE: PRT
ORGANISM: Humicola lanuginosa lipase
US-09-007-288E-145

Query Match 24.3%; Score 362; DB 4; Length 289;
Best Local Similarity 30.2%; Pred. No. 2e-29;
Matches 92; Conservative 58; Mismatches 105; Indels 50; Gaps 11;

QY 7 KHLVAVVVTAGHALAASQTGISEDLYSRLVEMATISQAAYADL-----CNIPST----- 55
DB 2 KRIGSLLGLSISALAEVSQLFNQNLFAQYSAAYCGKNDAPAGTNICTGNAC 61
QY 56 --IKGKIY-----NSQTDINGWILRDDSSKEIITVFRGTGSDTNQLDNTNYTLTPFD 107
DB 62 PEVEKADATFLYSPEDSGVDVTGFLDNTNKLIVLSFRGSRSIENWNLNPLDKEIN 121
QY 108 TLPQNCCEVHGYYIGWVSQVDOVESLVKQVQYDPYALTVTGHSLGASLAALTAQOL 167
DB 122 DI--CSCRGHDGFTSWRSVADTLROKVEDAVREHPDYRVVFTGHSLGGALATVAGADL 179
QY 168 SATYDNIRLVTGPRSGNQAFASYMNDAFQASSPDTTQ-----YFRVTHANDGIPNLPVPV 223
DB 180 RGNGYDIDVSYGAPRVGNRAFAEFL-----TVQTGTLRYIHTNDIVRPLPR 229
QY 224 EQGYAHGVEYV-----SVDPYSAQNTFVCTGDEVCCEAQGGQVNN-----AHTTYFGM 274
DB 230 EFGYSHSSPEWIKSGTLVPVT-RNDIV-----KIEGIDATGNNQNPIDIPAHLWYFGL 284
QY 275 TSGAC 279
DB 285 I-GTC 288

RESULT 5
US-08-434-255-13
Sequence 13, Application US/08434255
Patent No. 5621089
GENERAL INFORMATION:
APPLICANT: Sloma, Alan P.
APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Aaslyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5621089o No. 5621089disk of No. 5621089th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434.255
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Agria Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3764.400-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-434-255-13

Query Match 23.7%; Score 353.5; DB 1; Length 291;
Best Local Similarity 31.4%; Pred. No. 1.6e-28;
Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 12;

QY 14 VTAGHALAAS-TQGISDLYSRLVEMATISQAAYADL-----CNIPST-----IIKG 59
DB 10 VSAWTALASPIRREVSQLFNQNLFAQYSAAYCGKNDAPAGTNICTGNACPEVEKA 69
QY 60 EKIY-----NSQTDINGWILRDDSSKEIITVFRGTGSDTNQLDNTNYTLTPDTPQCN 113
DB 70 DATFLYSPEDSGVDVTGFLDNTNKLIVLSFRGSRSIENWNLNPLDKEINDI--CS 127
QY 114 GCEVHGYYIGWVSQVDOVESLVKQVQYDPYALTVTGHSLGASLAALTAQOLSATYDN 173
DB 128 GCRGHDGFTSWRSVADTLROKVEDAVREHPDYRVVFTGHSLGGALATVAGADLRNGYD 187
QY 174 IRLYTFGPRSGNQAFASYMNDAFQASSPDTTQ-----YFRVTHANDGIPNLPPEQGYAH 229
DB 188 IDVSYGAPRVGNRAFAEFL-----TVQTGTLRYIHTNDIVRPLPRPFGYSH 237
QY 230 GGYEYV-----SVDPYSAQNTFVCTGDEVCCEAQGGQVNN-----AHTTYGMSGAC 279
DB 238 SSPEYWKSGTLVPVT-RNDIV-----KIEGIDATGNNQNPIDIPAHLWYFGLI-GTC 290

RESULT 6
US-08-459-967-13
Sequence 13, Application US/08459967
Patent No. 5622841
GENERAL INFORMATION:
APPLICANT: Sloma, Alan P.
APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Aaslyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5622841o No. 5622841disk of No. 5622841th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459.967
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/434.255


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/ TELEPHONE: 212-867-0123
/ TELEFAX: 212-878-9655
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 291 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-459-871-13

Query Match      23.7%; Score 353.5; DB 1; Length 291;
Best Local Similarity 31.4%; Pred. No. 1.6e-28;
Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 12;

QY 14 VTAGHALAAS-TQGISDLYSLRLEMATISQAAYADL-----CNIPST-----IIKG 59
Db 10 VSAWTALASPIRREVSDLFNQFNLPFAQYSAAYCGKNDAPAGTNITCTGNACPEVEKA 69
QY 60 EKIV-----NSQTDINGWILRDDSSKEIITVFRGTGSDTNLQDNTYTLTPFDLPQCN 113
Db 70 DATFLYSFDSGVDVTGFLALDNTKLVLSFRGSRSIENWIGNLNFDLKEINDI--CS 127
QY 114 GCEVHGYYIGWVSQDOVESLVKQOVSQYDPDYALTVTGHSLSGLASLAALTAQOLSATYDN 173
Db 128 GCRGHDGFTSSWRSVADTLROKVEDAVREHPDYRVVFTGHSLSGLGALATVAGADLRNGYD 187
QY 174 IRLYTFGEPRSGNQAFASYMNDAPQASSPDITQ-----YFRVTHANDGIPNLPPEQGYAH 229
Db 188 IDVFSYGAPRVGNRAFAEFL-----TVQTGGTLRYITHNTNDIVPRLPPREFGYSH 237
QY 230 GGVEYW-----SVDPSYAQNTFVCTGDEVQCEAQQGGVNN-----AHTTYFGMTSGAC 279
Db 238 SSPEYIKSGTLVPVT-RNDIV-----KIEGIDATGNNQNPDPDIPAHLWTFGLI-GTC 290

RESULT 9
US-08-244-686-4
/ Sequence 4, Application US/08244686
/ Patent No. 5703358
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: Process for the production of a protein
/ TITLE OF INVENTION: using endoxylanase II (exla) expression signals
/ NUMBER OF SEQUENCES: 12
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA: US/08/244,686
/ APPLICATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 291 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-244-686-4

Query Match      23.7%; Score 353.5; DB 1; Length 291;
Best Local Similarity 31.4%; Pred. No. 1.6e-28;
Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 12;

QY 14 VTAGHALAAS-TQGISDLYSLRLEMATISQAAYADL-----CNIPST-----IIKG 59
Db 10 VSAWTALASPIRREVSDLFNQFNLPFAQYSAAYCGKNDAPAGTNITCTGNACPEVEKA 69
QY 60 EKIV-----NSQTDINGWILRDDSSKEIITVFRGTGSDTNLQDNTYTLTPFDLPQCN 113
Db 70 DATFLYSFDSGVDVTGFLALDNTKLVLSFRGSRSIENWIGNLNFDLKEINDI--CS 127
QY 114 GCEVHGYYIGWVSQDOVESLVKQOVSQYDPDYALTVTGHSLSGLASLAALTAQOLSATYDN 173
Db 128 GCRGHDGFTSSWRSVADTLROKVEDAVREHPDYRVVFTGHSLSGLGALATVAGADLRNGYD 187
QY 174 IRLYTFGEPRSGNQAFASYMNDAPQASSPDITQ-----YFRVTHANDGIPNLPPEQGYAH 229
Db 188 IDVFSYGAPRVGNRAFAEFL-----TVQTGGTLRYITHNTNDIVPRLPPREFGYSH 237
QY 230 GGVEYW-----SVDPSYAQNTFVCTGDEVQCEAQQGGVNN-----AHTTYFGMTSGAC 279
Db 238 SSPEYIKSGTLVPVT-RNDIV-----KIEGIDATGNNQNPDPDIPAHLWTFGLI-GTC 290

RESULT 9
US-08-244-686-4
/ Sequence 4, Application US/08244686
/ Patent No. 5703358
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: Process for the production of a protein
/ TITLE OF INVENTION: using endoxylanase II (exla) expression signals
/ NUMBER OF SEQUENCES: 12
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA: US/08/244,686
/ APPLICATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 291 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-244-686-4

Query Match      23.7%; Score 353.5; DB 2; Length 291;
Best Local Similarity 31.4%; Pred. No. 1.6e-28;
Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 12;

QY 14 VTAGHALAAS-TQGISDLYSLRLEMATISQAAYADL-----CNIPST-----IIKG 59
Db 10 VSAWTALASPIRREVSDLFNQFNLPFAQYSAAYCGKNDAPAGTNITCTGNACPEVEKA 69
QY 60 EKIV-----NSQTDINGWILRDDSSKEIITVFRGTGSDTNLQDNTYTLTPFDLPQCN 113
Db 70 DATFLYSFDSGVDVTGFLALDNTKLVLSFRGSRSIENWIGNLNFDLKEINDI--CS 127
QY 114 GCEVHGYYIGWVSQDOVESLVKQOVSQYDPDYALTVTGHSLSGLASLAALTAQOLSATYDN 173
Db 128 GCRGHDGFTSSWRSVADTLROKVEDAVREHPDYRVVFTGHSLSGLGALATVAGADLRNGYD 187
QY 174 IRLYTFGEPRSGNQAFASYMNDAPQASSPDITQ-----YFRVTHANDGIPNLPPEQGYAH 229
Db 188 IDVFSYGAPRVGNRAFAEFL-----TVQTGGTLRYITHNTNDIVPRLPPREFGYSH 237
QY 230 GGVEYW-----SVDPSYAQNTFVCTGDEVQCEAQQGGVNN-----AHTTYFGMTSGAC 279
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Db 238 SSPEYWKSTGLVPVT-RNDIV---KIEGIDATGNNQNPIDIPAHLMYFGLI-GTC 290

RESULT 11

US-08-921-426-10
; Sequence 10, Application US/08921426
; Patent No. 5837847
; GENERAL INFORMATION:
; APPLICANT: Royer, John C
; APPLICANT: Moyer, Donna L
; APPLICANT: Yoder, Wendy T
; APPLICANT: Shuster, Jeffrey R
; TITLE OF INVENTION: NON-TOXIC, NON-PATHOGENIC
; TITLE OF INVENTION: FUSARIUM EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5837847o No..5837847disk of No. 5837847th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/921,426
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/456,433
; FILING DATE: 01-JUN-1995
; APPLICATION NUMBER: US 08/404,678
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Agrie Dr., Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 4216.010-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-921-426-10

D6 238 SSPEYWKSGTILVPT-RNDIV-----KIEGIDATGGNNQNPIDIPAHLLWTFGLI-GTC 290

RESULT 12

US-08/479-275D-2
Sequence 2, Application US/08479275D
Patent No. 5869438
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Patkar, Shankant A.
APPLICANT: Gormsen, Erik
APPLICANT: Clausen, Ib G.
APPLICANT: Okkels, Jens S.
APPLICANT: Thellersen, Marianne
TITLE OF INVENTION: LIPASE VARIANTS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5869438o No. 5869438disk of No. 5869438th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,275D
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 510
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3520.514-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08/479-275D-2

RESULT 13

US-08-488-271B-2
; Sequence 2, Application US/08488271B
; Patent No. 5892013
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Patkar, Shankant A.
; APPLICANT: Gormsen, Erik
; APPLICANT: Clausen, Ib G.
; APPLICANT: Okkels, Jens S.
; APPLICANT: Thellersen, Marianne
; TITLE OF INVENTION: LIPASE VARIANTS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5892013 of No. 5892013disk of No. 5892013th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,271B
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3520.504-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-271B-2

Query Match 23.7%; Score 353.5; DB 2; Length 291;

Best Local Similarity 31.4%; Pred. No. 1.6e-28;

Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 12;

Qy 14 VTAGHALAAS-TQIGSEDLVSRVEMATISOAAAYADL-----CNIPST-----IIKG 59
Db 10 VSAWALASPIREVSODLFNQFNLFQYSAAYCGKKNADAPAGTNITCTGNACPEVEKA 69
Qy 60 EKIX-----NSQTDINGWILRDDSSKEIITVFRGTGSDTNLQDNTNLTPTPDLPCQN 113
Db 70 DATFLYSFEDSGVDVTGFLALDNTNKLIVLSFRGSRSIENWIGNLFDLKEINDI--CS 127
Qy 114 GCEVHGYYIGWVSQDVQVESLVKQVQSPDYALTVTGHSLGASLAALTAQOLSATYDN 173
Db 128 GCRGHDGFTSSWRSVADTLRQKVEDAVREHPDYRVVFTGSHLGGALATVAGADLRNGYD 187
Qy 174 IRLYTFGERPSGNOAFASYNDFAQSSPDPTQ-----YFRVTHANDGIPNLPVPEQGYAH 229
Db 188 IDVFSYGAPRVGNRAFAEFL-----TVQGTGLYRITHNTNDIVPRLPPEFGYSH 237
Qy 230 GGVEYH----SVDPSYAQNTFVCTGDEVQCEAGGQGVNN-----AHTTYFGMTSGAC 279
Db 238 SSPEYIKSGTLVPVT-RNDIV-----KIEGIDATGGNNQNPIDIPAHLYWFGLI-GTC 290

RESULT 14

US-08-140-008A-2
; Sequence 2, Application US/08140008A
; Patent No. 5914306

GENERAL INFORMATION:

; APPLICANT: SVENDSEN, Allan
; APPLICANT: VON DER OSTEN, Claus
; APPLICANT: CLAUSEN, Ib Groth
; APPLICANT: PATKAR, Shankant Anant
; APPLICANT: BORCH, Kim
; TITLE OF INVENTION: STABILIZED ENZYMES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5914306 of No. 5914306disk of No. 5914306th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/140,008A
; FILING DATE: 22-OCT-1993
; CLASSIFICATION: 252
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3601.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-140-008A-2

Query Match 23.7%; Score 353.5; DB 2; Length 291;

Best Local Similarity 31.4%; Pred. No. 1.6e-28;

Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 12;

Qy 14 VTAGHALAAS-TQIGSEDLVSRVEMATISOAAAYADL-----CNIPST-----IIKG 59
Db 10 VSAWALASPIREVSODLFNQFNLFQYSAAYCGKKNADAPAGTNITCTGNACPEVEKA 69
Qy 60 EKIX-----NSQTDINGWILRDDSSKEIITVFRGTGSDTNLQDNTNLTPTPDLPCQN 113
Db 70 DATFLYSFEDSGVDVTGFLALDNTNKLIVLSFRGSRSIENWIGNLFDLKEINDI--CS 127
Qy 114 GCEVHGYYIGWVSQDVQVESLVKQVQSPDYALTVTGHSLGASLAALTAQOLSATYDN 173
Db 128 GCRGHDGFTSSWRSVADTLRQKVEDAVREHPDYRVVFTGSHLGGALATVAGADLRNGYD 187
Qy 174 IRLYTFGERPSGNOAFASYNDFAQSSPDPTQ-----YFRVTHANDGIPNLPVPEQGYAH 229
Db 188 IDVFSYGAPRVGNRAFAEFL-----TVQGTGLYRITHNTNDIVPRLPPEFGYSH 237
Qy 230 GGVEYH----SVDPSYAQNTFVCTGDEVQCEAGGQGVNN-----AHTTYFGMTSGAC 279
Db 238 SSPEYIKSGTLVPVT-RNDIV-----KIEGIDATGGNNQNPIDIPAHLYWFGLI-GTC 290

RESULT 15

US-08-701-339-2
; Sequence 2, Application US/08701339
; Patent No. 5976855
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Clausen, Ib
; APPLICANT: Okkels, Jens
; APPLICANT: Thellersen, Marianne

;; TITLE OF INVENTION: A Method of Preparing A Variant of A
;; TITLE OF INVENTION: Lipolytic Enzyme
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: No. 59768550 No. 5976855disk of No. 5976855th America, Inc.
;; STREET: 405 Lexington Avenue, 64th Floor
;; CITY: New York
;; STATE: New York
;; COUNTRY: United States of America
;; ZIP: 10174-6401
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/701,339
;; FILING DATE: 22-AUG-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lambiris, Elias J.
;; REGISTRATION NUMBER: 33,728
;; REFERENCE/DOCKET NUMBER: 4153.204-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-867-0123
;; TELEFAX: 212-878-9655
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 291 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-701-339-2

Query Match 23.7%; Score 353.5; DB 2; Length 291;
Best Local Similarity 31.4%; Pred. No. 1.6e-28;
Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 12;
QY 14 VTAGHALAAS-TQGISDLYSLVEMATISQAAYADL-----CNIPST-----IIKG 59
DB 10 VSAWTALASPIREVSQDLFNQFNLFQAQYSAAYCGKNDAPAGTNTCTGNACREVEKA 69
QY 60 EKIIY-----NSQTDINGWILRDDSSKEIITVPRGTGSDTNLQLDNTNYLTTPDTELPQC 113
DB 70 DATFLYSFEDSGVDVTGFLALDNTNKLIVLSFRGSRSIENWICNLNFDLKEINDI--CS 127
QY 114 GCEVHGGYIGVSVQDOVESLYKQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 173
DB 128 GCRGHDGFTSSWRKSVADTLRQKVEDAVREHPDYRVVFTGSHLGLALATVAGDLRNGYD 187
QY 174 IRLYTFGEPRSGNQAFASYNDAFOASSPDTTQ----YFRVTHANDGIPNLPPVQGYAH 229
DB 188 IDVFSYGARVGNRAEFL-----TVOTGGTLYRITHNDIVPLPRFGYSH 237
QY 230 GGVEYH-----SVDPPSAQNTFVCTGDEVQCCCEAGQGGVNN-----AHTYFGMTSGAC 279
DB 238 SPPEYWKSGTLVPVT-RNDIV---KIEGIDATGNGNQPNIPIPAHLWYFGLI-GTC 290

Search completed: December 17, 2003, 15:43:37
Job time : 22 secs

PT photoprotective or antiinflammatory agents
 XX Claim 8; Fig 5A-B; 40pp; English.
 XX
 CC This polypeptide comprises a novel 38 kDa methyl ferulate esterase
 CC (FAE) of *Aspergillus niger*. Its amino acid sequence was deduced
 CC from a 2436 bp genomic DNA sequence (see AAV28496). The invention
 CC provides vectors that include the DNA sequence, host cells
 CC transformed with the DNA or vectors, fermentation broths comprising
 CC such host cells, and esterase proteins expressed by the host cells.
 CC The FAE can cleave the ester linkage of phenolic esters. It can be
 CC used in a claimed feed supplement and in a claimed process of
 CC treating fabric, yarn or textiles. It can also be used in the pulp
 CC and paper industry, for the synthesis of carbohydrate derivatives
 CC and in the bioconversion of agricultural residue to fermentable
 CC sugars and free phenolic acid useful e.g. as an antioxidant,
 CC photoprotective, antimicrobial or antiinflammatory agent in foods
 CC and personal care products, feedstock for conversion to flavours
 CC (e.g. vanillin), biopolymers and valuable chemicals. It can also
 CC be used in the modification of polysaccharides, e.g. gums, to
 CC generate new properties, and in the processing of grain.
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 1492; DB 19; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.6e-130; Indels 0; Gaps 0;
 Matches 281; Conservative 0; Mismatches 0;
 QY 1 MKQFSKXHLVAVVVTAGHALAASQTQISEDLVSRVEMATISQAAYADLCNIPSTIIKGE 60
 DB 1 MKQFSKXHLVAVVVTAGHALAASQTQISEDLVSRVEMATISQAAYADLCNIPSTIIKGE 60
 QY 61 KIYNSQTDINGWILRDDSSKEIITVPRGTGSDTNLQLDNTYTLTPPDTLPQCNGCEVHGG 120
 DB 61 KIYNSQTDINGWILRDDSSKEIITVPRGTGSDTNLQLDNTYTLTPPDTLPQCNGCEVHGG 120
 QY 121 YVIGWVSQDOVESLVKQVSYQPDYALVTGHSGLASLAALTAQLSATYDNIIRLYTFG 180
 DB 121 YVIGWVSQDOVESLVKQVSYQPDYALVTGHSGLASLAALTAQLSATYDNIIRLYTFG 180
 QY 181 EPRSGNQAFASYMNDAFQASSPDTTQYFRVTHANDGIPNLPVVEQYAHGGVEYWSVDPY 240
 DB 181 EPRSGNQAFASYMNDAFQASSPDTTQYFRVTHANDGIPNLPVVEQYAHGGVEYWSVDPY 240
 QY 241 SAQNTFVCTGDEVQCCAGCGGQVNNHAHTTYFGMTSGACTW 281
 DB 241 SAQNTFVCTGDEVQCCAGCGGQVNNHAHTTYFGMTSGACTW 281
 RESULT 2
 AAW56727
 ID AAW56727 standard; Protein; 197 AA.
 AC AAW56727;
 XX
 XX 28-AUG-1998 (first entry)
 DT
 DE *Aspergillus niger* ferulic acid esterase fragment.
 KW Ferulic acid esterase; esterolytic enzyme; feed supplement;
 KW fabric; yarn; textile.
 OS
 OS *Aspergillus niger*.
 XX
 XX WO9814594-A2.
 PN
 XX
 PD 09-APR-1998.
 XX
 XX 29-SEP-1997; 97WO-US17614.
 PF
 XX 30-SEP-1996; 96US-0722713.
 PR
 XX (GENV) GENENCOOR INT INC.
 PA

XX Borneman WS, Bower BS;
 XX
 XX WPI; 1998-240093/21.
 DR N-P8DB; AAV28495.
 XX
 XX New esterase from *Aspergillus niger* - useful for, e.g. feed and food
 XX processing, treating fabrics or for producing antioxidant,
 XX photoprotective or antiinflammatory agents
 PS Example 2; Fig 2; 40pp; English.
 XX
 CC This polypeptide comprises a portion of a novel 38 kDa methyl
 CC ferulate esterase (FAE, see AAW56728) of *Aspergillus niger*. Its
 CC amino acid sequence was deduced from a 650 bp DNA fragment (see
 CC AAV28495) obtained by PCR amplification of *A. niger* genomic DNA.
 CC The FAE can cleave the ester linkage of phenolic esters. It
 CC can be expressed in host cells and used in a claimed feed
 CC supplement and in a claimed process for treating fabric, yarn or
 CC textiles.
 XX
 SQ Sequence 197 AA;
 Query Match 68.8%; Score 1026; DB 19; Length 197;
 Best Local Similarity 100.0%; Pred. No. 3.5e-87;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 ASTQGISDLYSRVEMATISQAAYADLCNIPSTIIKGEKIYNSQTDINGWILRDDSSKE 81
 DB 1 ASTQGISDLYSRVEMATISQAAYADLCNIPSTIIKGEKIYNSQTDINGWILRDDSSKE 60
 QY 82 IITVFRGTGSDTNLQLDNTYTLTPPDTLPQCNGCEVHGGYVIGWVSQDOVESLVKQVVS 141
 DB 61 IITVFRGTGSDTNLQLDNTYTLTPPDTLPQCNGCEVHGGYVIGWVSQDOVESLVKQVVS 120
 QY 142 QYPDYALVTGHSGLASLAALTAQLSATYDNIIRLYTFGPRSGNQAFASYMNDAFQASS 201
 DB 121 QYPDYALVTGHSGLASLAALTAQLSATYDNIIRLYTFGPRSGNQAFASYMNDAFQASS 180
 QY 202 PDDTQYFRVTHANDGIP 218
 DB 181 PDDTQYFRVTHANDGIP 197
 RESULT 3
 AAW19713
 ID AAW19713 standard; peptide; 77 AA.
 AC AAW19713;
 XX
 XX 04-AUG-1997 (first entry)
 DT
 DE Ferulic acid esterase fragment #4.
 XX
 XX Ferulic acid esterase; FAE; enzyme system; plant; wheat bran; sugar beet;
 KW water insoluble pentosan; corn cobs; dough; lignin; terpenoid; vanillin;
 KW antioxidant; oxidative agent stabiliser; enzyme; cell wall breakdown;
 KW nutrient absorption; growth rate; feed utilisation; xylanase.
 XX
 OS *Aspergillus niger* strain 3M43.
 XX
 XX GB2301103-A.
 PN
 XX 27-NOV-1996.
 XX
 XX 23-MAY-1995; 95GB-0010370.
 PF
 XX 23-MAY-1995; 95GB-0010370.
 PR
 XX (DANI-) DANISCO AS.
 PA
 XX De Vries RP, Michelsen B, Poulsen CH, Soe JB, Visser J;
 PI Zargahi MR;

XX WPI; 1996-508189/51.
 DR N-PSDB; AAT43178.
 XX
 PT Enzyme system including ferulic acid esterase - for treating plant
 PT material, esp. food and feed, to release ferulic acid, improving
 PT nutrient absorption
 XX
 PS Claim 1; Page 53; 63pp; English.
 XX
 CC AAU19710-W19713 represent fragments of the ferulic acid esterase (FAE)
 CC used in the enzyme system of the invention. The enzyme system also
 CC includes at least one protein or enzyme of interest. The enzyme system,
 CC or recombinant FAE, are used to release a phenolic acid, especially
 CC ferulic acid (FA), from a substrate, particularly a plant material such
 CC as wheat bran or water insoluble pentosan, sugar beet or corn cobs,
 CC preferably in the form of food or feed. Particularly the material is a
 CC dough for making baked goods. Also, FAE can be used to treat paper or
 CC pulp to improve removal of lignin and terpenoids. The FA released can be
 CC used to prepare flavourings, specifically vanillin, as an in situ
 CC antioxidant, or as an in situ stabiliser of oxidative agents, e.g.
 CC enzymes. Treatment with FAE significantly improves breakdown of plant
 CC cell walls so improves nutrient absorption and thus growth rate and/or
 CC feed utilisation in animals. When used with xylanase, FAE shows a
 CC synergistic effect.
 XX
 SQ Sequence 77 AA;
 Query Match 27.0%; Score 403; DB 17; Length 77;
 Best Local Similarity 94.8%; Pred. No. 8e-30;
 Matches 73; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 69 INGTLRDSSKEIITVFRGTGSDTNLQLDNTYLTPTPTLPCNCGEVHGGYIGWISV 128
 Db 1 INGTLRDTSKEIITVFRGTGSDTNLQLDNTYLTPTPTLPCNCGEVHGGYIGWISV 60
 QY 129 QDQVESLVKQVQSYPD 145
 Db 61 QDQVESLVKQASQYPD 77
 RESULT 4
 AAW58541
 ID AAW58541 standard; Protein; 295 AA.
 XX
 AC AAW58541;
 XX
 DT 02-SEP-1998 (first entry)
 XX
 DE Aspergillus oryzae phospholipase A1.
 XX
 KW Aspergillus oryzae; phospholipase A1; microbe; PLA1.
 XX
 OS Aspergillus oryzae.
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..26
 FT /label= signal
 FT Protein 27..295
 FT /label= phospholipase_A1
 XX
 PN JP10155493-A.
 XX
 PD 16-JUN-1998.
 XX
 PF 03-OCT-1997; 97JP-0270967.
 XX
 PR 04-OCT-1996; 96JP-0264241.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI; 1998-391046/34.
 DR N-PSDB; AAV31126.

XX Aspergillus-derived phospholipase A1 gene - used for the recombinant
 PT production of phospholipase A of high purity and in a high yield
 XX
 PS Claim 2; Page 17-18; 23pp; Japanese.
 XX
 CC The present sequence represents phospholipase A1 (PLA1) derived from
 CC Aspergillus oryzae. Phospholipase A can be prepared by culturing
 CC host cells and collecting the host cell from the culture. DNA
 CC encoding mature PLA1 can be used to produce recombinant phospholipase
 CC A of high purity and in a high yield.
 XX
 SQ Sequence 295 AA;
 Query Match 24.7%; Score 368.5; DB 19; Length 295;
 Best Local Similarity 33.0%; Pred. No. 9.1e-26;
 Matches 97; Conservative 47; Mismatches 105; Indels 45; Gaps 10;
 QY 9 VLAVVVTAGHALAASQTGISEDLYSLVEMATISQAAYADLCNIPSTIIKGEKI----- 62
 Db 10 VAGLFLLAQAAPASLRDVSLSLLNLDLFAQYSAAYCDE-NLNST---GTKLTCVGN 65
 QY 63 -----YNSQTDIN---QWILRDDSKEIITVFRGTGSDTNLQLDNTYLTPT 105
 Db 66 CPLVEAASQTSLDEFNNESSYGNPAGYLAADETNKLVLFSRGSADLANVWNLFGLE- 124
 QY 106 FDTLPQCNCGEVHGGYIGWISVQDQVESLVKQVQSYPDYALTVTCHSLGASLAALTA 165
 Db 125 -DASDLCSGCEVHSGFWKAWSEIADTITSKVESALSDHSDYSLVLTGHSYGAALAA 183
 QY 166 QLSATVDNRLTYTFGRGNQAFASYMNDAFQASSPDTTQYFRVTHANDGIPNLPV 225
 Db 184 ALRNSGSHVELNYGQPLGNEALATYITDQNGKN-----YRVTHNDIVPKLP 237
 QY 226 GYAHGGEVYMSVDPYSAQNTFVCTGD--EYQCCQAQGG-----QGVN-NAHTTYF 272
 Db 238 GYHHSPEYI---SSADEATVTTTDTVTEVTGIDATGNDGTGTSIDAHRYWF 288
 RESULT 5
 AAW23217
 ID AAW23217 standard; Protein; 289 AA.
 XX
 AC AAW23217;
 XX
 DT 29-OCT-1997 (first entry)
 XX
 DE Product of Humicola lanuginosa lipase gene as present in psX581.
 XX
 KW Lipolytic enzyme; lipase; chimeric.
 XX
 OS Chimeric - Humicola lanuginosa.
 OS Chimeric - Aspergillus lyticus.
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= sig_peptide
 FT Peptide 21..289
 FT /label= mat_peptide
 XX
 PN WO9704078-A1.
 XX
 PD 06-FEB-1997.
 XX
 PF 12-JUL-1996; 96WO-DK00321.
 XX
 PR 01-APR-1996; 96DK-0000372.
 PR 14-JUL-1995; 95DK-0000832.
 PR 13-SEP-1995; 95DK-0001013.
 PR 29-SEP-1995; 95DK-0001096.
 PR 21-NOV-1995; 95DK-0001306.
 PR 14-FEB-1996; 96US-0011634.

XX (NOVO) NOVO-NORDISK AS.
 XX Fuglsang CC, Halkier T, Jorgensen ST, Okkels JS;
 PI Patkar SA, Petersen DA, Thellersen M, Vind J;
 XX WPI; 1997-132621/12.
 DR N-PSDB; AAT68728.
 XX Modified lipolytic enzymes with peptide extensions at one or both
 PT ends - esp. for use in detergent and dishwashing compsn., have
 PT improved substrate affinity, stability and wash performance
 XX Example 5; Fig 3; 197pp; English.
 XX The present sequence is the product of the coding region of the
 CC Humicola lanuginosa lipase gene as present in the E. coli
 CC expression vector pSX581. The signal sequence is the Aspergillus
 CC lyticus protease I signal and Glu21 is the 1st amino acid residue
 CC of the parent lipase.
 XX SQ Sequence 289 AA;
 Query Match 24.3%; Score 362; DB 18; Length 289;
 Best Local Similarity 30.2%; Pred. No. 3.6e-25;
 Matches 92; Conservative 58; Mismatches 105; Indels 50; Gaps 11;
 QY 7 KHLVAVVTAGHALAASTQGISDLYSLVEMATISQAAYADL-----CNIPST---- 55
 Db 2 KRICGSLLLGLSISAALAEVSQDLFNQFNLPAQYSAAYCGKNNDAPAGTNTCTGNAC 61
 QY 56 --IIKGEKIY-----NSQTDINGWILRDDSSKEITVFRGTGSDTNLQDNTYLTTPFD 107
 Db 62 PEVEKADATFLYSFEDSGVGDVTGFLALDNTNKLIVLSFRGSRSIENWIGNLNFDLKEIN 121
 QY 108 TLPQNGCEVHGYYIGWVSQDQVSLVKQVQSOYPDYALTVTGHSLSGLASLAALTAQAL 167
 Db 122 DI--CSGCRGHGFTSSWSRVAATLQKQVEDAVREHPDYRVVFTGHSLSGLALATVAGADL 179
 QY 168 SATYDNIRLYTFGEPRSGNOAFASYMNDAPQASSPDTTQ-----YFRVTHANDGIPNLPV 223
 Db 180 RGNVDIDVFSYGAPRVGNRAFAEFL-----TVQTGGTLYRITHNDIVRPLPPR 229
 QY 224 EGYANGGVVEYW-----SVDPYSAQNTFVCTGDEVQCEAGGOGGVN-----AHTTYFGM 274
 Db 230 EFGYSHSSPEYWKSGTLVPVT-RNDIV-----KIEGIDATGNNQNPIDIPAHLMVYFGL 284
 QY 275 TSGAC 279
 Db 285 I-GTC 288
 RESULT 6
 ID AAW19647
 AC AAW19647 standard; Protein; 289 AA.
 XX AAW19647;
 XX Humicola lanuginosa modified lipase.
 DT 04-SEP-1997 (first entry)
 XX Humicola lanuginosa
 DE Lipase; lipolytic enzyme; protein engineering; detergent;
 KW psx581.
 KW Chimeric Humicola lanuginosa DSM4109;
 XX Chimeric Aspergillus lyticus;
 OS Key Location/Qualifiers
 FH 1..20
 FT Peptide /label= sig_peptide
 FT /note= "A. lyticus protease I signal"
 FT 21..289

PT /label= Mat_protein
 XX /note= "native mature enzyme"
 PN W09704079-A1.
 XX 06-FEB-1997.
 PD 12-JUL-1996; 96WO-DK00322.
 XX 07-MAY-1996; 96US-0020461.
 PR 14-JUL-1995; 95DK-0000832.
 PR 13-SEP-1995; 95DK-0001013.
 PR 29-SEP-1995; 95DK-0001096.
 PR 21-NOV-1995; 95DK-0001306.
 PR 14-FEB-1996; 96US-0011634.
 PR 01-APR-1996; 96DK-0000372.
 XX (NOVO) NOVO-NORDISK AS.
 PA Fuglsang CC, Halkier T, Jorgensen ST, Okkels JS;
 XX Patkar SA, Petersen DA, Thellersen M, Vind J;
 PI WPI; 1997-132622/12.
 DR N-PSDB; AAT68728.
 XX Modified lipolytic enzymes with peptide extensions at one or both
 PT ends - useful in detergent and dishwashing compsn., have improved
 PT substrate affinity, stability and wash performance
 XX Example 4; Fig 3; 191pp; English.
 XX A modified lipase (AAW19647) comprises an Aspergillus lyticus
 CC protease I signal and the mature protein sequence of Humicola
 CC lanuginosa lipase. It is encoded by a DNA sequence (AAT68728)
 CC present in E. coli expression vector pSX581. E. coli W3110 lacI1
 CC (pSX581) transformants produced a lipase that showed no improvement
 CC in wash performance over the native H. lanuginosa enzyme. Addition
 CC of an N-terminal 5-amino acid extension (see also AAW19646) improved
 CC wash performance 2-fold.
 XX SQ Sequence 289 AA;
 Query Match 24.3%; Score 362; DB 18; Length 289;
 Best Local Similarity 30.2%; Pred. No. 3.6e-25;
 Matches 92; Conservative 58; Mismatches 105; Indels 50; Gaps 11;
 QY 7 KHLVAVVTAGHALAASTQGISDLYSLVEMATISQAAYADL-----CNIPST---- 55
 Db 2 KRICGSLLLGLSISAALAEVSQDLFNQFNLPAQYSAAYCGKNNDAPAGTNTCTGNAC 61
 QY 56 --IIKGEKIY-----NSQTDINGWILRDDSSKEITVFRGTGSDTNLQDNTYLTTPFD 107
 Db 62 PEVEKADATFLYSFEDSGVGDVTGFLALDNTNKLIVLSFRGSRSIENWIGNLNFDLKEIN 121
 QY 108 TLPQNGCEVHGYYIGWVSQDQVSLVKQVQSOYPDYALTVTGHSLSGLASLAALTAQAL 167
 Db 122 DI--CSGCRGHGFTSSWSRVAATLQKQVEDAVREHPDYRVVFTGHSLSGLALATVAGADL 179
 QY 168 SATYDNIRLYTFGEPRSGNOAFASYMNDAPQASSPDTTQ-----YFRVTHANDGIPNLPV 223
 Db 180 RGNVDIDVFSYGAPRVGNRAFAEFL-----TVQTGGTLYRITHNDIVRPLPPR 229
 QY 224 EGYANGGVVEYW-----SVDPYSAQNTFVCTGDEVQCEAGGOGGVN-----AHTTYFGM 274
 Db 230 EFGYSHSSPEYWKSGTLVPVT-RNDIV-----KIEGIDATGNNQNPIDIPAHLMVYFGL 284
 QY 275 TSGAC 279
 Db 285 I-GTC 288
 RESULT 7
 ABG22582

ID	ABG32582	standard; Protein; 269 AA.	CC	sequence given on pages 20-21 of the specification.
XX	AC	ABG32582;	XX	
XX	DT	15-NOV-2002 (first entry)	SQ	Sequence 269 AA;
XX	DE	Thermomyces lanuginosus lipolytic enzyme variant #30.		
XX	KW	Fungal; lipolytic; enzyme; pitch trouble; mechanical pulp; paper-making;		Query Match 24.2%; Score 361; DB 23; Length 269;
XX	KW	dough; baked product; fabric; pasta; noodle; detergent additive; leather;		Best Local Similarity 31.4%; Pred. No. 4e-25;
XX	KW	crumb structure; soft dough; elasticity; extensibility; variant.		Matches 89; Conservative 47; Mismatches 101; Indels 46; Gaps 9;
XX	OS	Thermomyces lanuginosus.		
XX	FT	Key Location/Qualifiers		
XX	FT	Misc-difference 27 /note= "Asp substituted by Arg"		
XX	FT	Misc-difference 38 /note= "Gly substituted by Cys"		
XX	FT	Misc-difference 111 /note= "Asp substituted by Gly"		
XX	FT	Misc-difference 216 /note= "Ser substituted by Pro"		
XX	FT	Misc-difference 227 /note= "Leu substituted by Gly"		
XX	FT	Misc-difference 256 /note= "Pro substituted by Thr"		
XX	PN	WO200255679-A2.		
XX	PD	18-JUL-2002.		
XX	PF	10-JAN-2002; 2002WO-DK00016.		
XX	PR	10-JAN-2001; 2001DK-0000032.		
XX	PR	18-JAN-2001; 2001US-262579P.		
XX	PA	(NOVO) NOVOZYMES AS.		
XX	PI	Minning S, Vind-J, Glad SOS, Danielsen S, Borch K;		
XX	XX	WPI; 2002-619105/66.		
XX	XX	New variants of fungal lipolytic enzymes with improved thermostability		
XX	XX	useful for hydrolysing a carboxylic ester, controlling pitch troubles		
XX	XX	in mechanical pulp production or paper-making process and for preparing		
XX	XX	dough		
XX	XX	Claim 10; Page -: 29pp; English.		
XX	XX	The present invention relates to a new variant of a parent fungal		
XX	XX	lipolytic enzyme. The invention comprises an amino acid sequence which		
XX	XX	compared to the parent lipolytic enzyme comprises substitution of an		
XX	XX	amino acid residue and which is more thermostable than the parent		
XX	XX	lipolytic enzyme. The invention is useful for hydrolysing a carboxylic		
XX	XX	acid ester, by incubating the ester with the lipase in the presence of		
XX	XX	water, and for controlling pitch troubles in a process for the production		
XX	XX	of mechanical pulp or a paper-making process using mechanical pulp. The		
XX	XX	invention is also useful for preparing a dough or a baked product		
XX	XX	prepared from the dough, and for hydrolysing, synthesising or		
XX	XX	interesterifying an ester, by reacting the ester with water, reacting an		
XX	XX	acid with an alcohol or interesterifying the ester with an acid, an		
XX	XX	alcohol or a second ester in the presence of the invention, and also for		
XX	XX	enzymatic removal of hydrophobic esters from fabrics. The invention is		
XX	XX	further useful for preparing a baked product, e.g. pasta or noodles, as a		
XX	XX	detergent additive and in leather industry. The invention is at least 4		
XX	XX	plusOC more thermostable than the parent lipolytic enzyme. The addition		
XX	XX	of the invention improves crumb structure of the baked product, and dough		
XX	XX	properties e.g. a less soft dough, higher elasticity and lower		
XX	XX	extensibility. The present amino acid sequence represents a Thermomyces		
XX	XX	lanuginosus lipolytic enzyme variant of the invention.		
XX	XX	Note: The present sequence is not shown in the specification but is		
XX	XX	derived from the Thermomyces lanuginosus lipolytic enzyme (ABG32551)		

RESULT 8

ABG32579

ID ABG32579 standard; Protein; 269 AA.

XX AC ABG32579;

XX DT 15-NOV-2002 (first entry)

XX DE Thermomyces lanuginosus lipolytic enzyme variant #27.

XX KW Fungal; lipolytic; enzyme; pitch trouble; mechanical pulp; paper-making;

XX KW dough; baked product; fabric; pasta; noodle; detergent additive; leather;

XX KW crumb structure; soft dough; elasticity; extensibility; variant.

XX OS Thermomyces lanuginosus.

XX FT Key Location/Qualifiers

XX FT Misc-difference 27 /note= "Asp substituted by Arg"

XX FT Misc-difference 111 /note= "Asp substituted by Gly"

XX FT Misc-difference 216 /note= "Ser substituted by Pro"

XX FT Misc-difference 225 /note= "Gly substituted by Pro"

XX FT Misc-difference 227 /note= "Leu substituted by Gly"

XX FT Misc-difference 256 /note= "Pro substituted by Thr"

XX PN WO200255679-A2.

XX PD 18-JUL-2002.

XX PF 10-JAN-2002; 2002WO-DK00016.

XX PR 10-JAN-2001; 2001DK-0000032.

XX PR 18-JAN-2001; 2001US-262579P.

XX PA (NOVO) NOVOZYMES AS.

XX PI Minning S, Vind-J, Glad SOS, Danielsen S, Borch K;

XX XX WPI; 2002-619105/66.

XX XX New variants of fungal lipolytic enzymes with improved thermostability

XX XX useful for hydrolysing a carboxylic ester, controlling pitch troubles

XX XX in mechanical pulp production or paper-making process and for preparing

XX XX dough

XX XX Claim 10; Page -: 29pp; English.

XX XX The present invention relates to a new variant of a parent fungal

XX XX lipolytic enzyme. The invention comprises an amino acid sequence which

XX XX compared to the parent lipolytic enzyme comprises substitution of an

XX XX amino acid residue and which is more thermostable than the parent

XX XX lipolytic enzyme. The invention is useful for hydrolysing a carboxylic

XX XX acid ester, by incubating the ester with the lipase in the presence of

XX XX water, and for controlling pitch troubles in a process for the production

XX XX of mechanical pulp or a paper-making process using mechanical pulp. The

XX XX invention is also useful for preparing a dough or a baked product

XX XX prepared from the dough, and for hydrolysing, synthesising or

XX XX interesterifying an ester, by reacting the ester with water, reacting an

XX XX acid with an alcohol or interesterifying the ester with an acid, an

XX XX alcohol or a second ester in the presence of the invention, and also for

XX XX enzymatic removal of hydrophobic esters from fabrics. The invention is

XX XX further useful for preparing a baked product, e.g. pasta or noodles, as a

XX XX detergent additive and in leather industry. The invention is at least 4

XX XX plusOC more thermostable than the parent lipolytic enzyme. The addition

XX XX of the invention improves crumb structure of the baked product, and dough

XX XX properties e.g. a less soft dough, higher elasticity and lower

XX XX extensibility. The present amino acid sequence represents a Thermomyces

XX XX lanuginosus lipolytic enzyme variant of the invention.

XX XX Note: The present sequence is not shown in the specification but is

XX XX derived from the Thermomyces lanuginosus lipolytic enzyme (ABG32551)

XX	AC	ABG32579	standard; Protein; 269 AA.	CC	sequence given on pages 20-21 of the specification.
XX	DT	15-NOV-2002 (first entry)	XX		
XX	DE	Thermomyces lanuginosus lipolytic enzyme variant #27.	SQ	Sequence 269 AA;	
XX	KW	Fungal; lipolytic; enzyme; pitch trouble; mechanical pulp; paper-making;			Query Match 24.2%; Score 361; DB 23; Length 269;
XX	KW	dough; baked product; fabric; pasta; noodle; detergent additive; leather;			Best Local Similarity 31.4%; Pred. No. 4e-25;
XX	KW	crumb structure; soft dough; elasticity; extensibility; variant.			Matches 89; Conservative 47; Mismatches 101; Indels 46; Gaps 9;
XX	OS	Thermomyces lanuginosus.			
XX	FT	Key Location/Qualifiers			
XX	FT	Misc-difference 27 /note= "Asp substituted by Arg"			
XX	FT	Misc-difference 111 /note= "Asp substituted by Gly"			
XX	FT	Misc-difference 216 /note= "Ser substituted by Pro"			
XX	FT	Misc-difference 225 /note= "Gly substituted by Pro"			
XX	FT	Misc-difference 227 /note= "Leu substituted by Gly"			
XX	FT	Misc-difference 256 /note= "Pro substituted by Thr"			
XX	PN	WO200255679-A2.			
XX	PD	18-JUL-2002.			
XX	PF	10-JAN-2002; 2002WO-DK00016.			
XX	PR	10-JAN-2001; 2001DK-0000032.			
XX	PR	18-JAN-2001; 2001US-262579P.			
XX	PA	(NOVO) NOVOZYMES AS.			
XX	PI	Minning S, Vind J, Glad SOS, Danielsen S, Borch K;			
XX	XX	WPI; 2002-619105/66.			

RESULT 8

ABG32579

ID ABG32579 standard; Protein; 269 AA.

XX AC ABG32579;

XX DT 15-NOV-2002 (first entry)

XX DE Thermomyces lanuginosus lipolytic enzyme variant #27.

XX KW Fungal; lipolytic; enzyme; pitch trouble; mechanical pulp; paper-making;

XX KW dough; baked product; fabric; pasta; noodle; detergent additive; leather;

XX KW crumb structure; soft dough; elasticity; extensibility; variant.

XX OS Thermomyces lanuginosus.

XX FT Key Location/Qualifiers

XX FT Misc-difference 27 /note= "Asp substituted by Arg"

XX FT Misc-difference 111 /note= "Asp substituted by Gly"

XX FT Misc-difference 216 /note= "Ser substituted by Pro"

XX FT Misc-difference 225 /note= "Gly substituted by Pro"

XX FT Misc-difference 227 /note= "Leu substituted by Gly"

XX FT Misc-difference 256 /note= "Pro substituted by Thr"

XX PN WO200255679-A2.

XX PD 18-JUL-2002.

XX PF 10-JAN-2002; 2002WO-DK00016.

XX PR 10-JAN-2001; 2001DK-0000032.

XX PR 18-JAN-2001; 2001US-262579P.

XX PA (NOVO) NOVOZYMES AS.

XX PI Minning S, Vind J, Glad SOS, Danielsen S, Borch K;

XX XX WPI; 2002-619105/66.

XX New variants of fungal lipolytic enzymes with improved thermostability
PT useful for hydrolysing a carboxylic ester, controlling pitch troubles
PT in mechanical pulp production or paper-making process and for preparing
PT dough
XX
XX
XX Claim 10; Page -: 29pp; English.
XX
XX The present invention relates to a new variant of a parent fungal
CC lipolytic enzyme. The invention comprises an amino acid sequence which
CC compared to the parent lipolytic enzyme comprises substitution of an
CC amino acid residue and which is more thermostable than the parent
CC lipolytic enzyme. The invention is useful for hydrolysing a carboxylic
CC acid ester, by incubating the ester with the lipase in the presence of
CC water, and for controlling pitch troubles in a process for the production
CC of mechanical pulp or a paper-making process using mechanical pulp. The
CC invention is also useful for preparing a dough or a baked product
CC prepared from the dough, and for hydrolysing, synthesising or
CC interesterifying as ester, by reacting the ester with water, reacting an
CC acid with an alcohol or interesterifying the ester with an acid, an
CC alcohol or a second ester in the presence of the invention, and also for
CC enzymatic removal of hydrophobic esters from fabrics. The invention is
CC further useful for preparing a baked product, e.g. pasta or noodles, as a
CC detergent additive and in leather industry. The invention is at least 4
CC plusOC more thermostable than the parent lipolytic enzyme. The addition
CC of the invention improves crumb structure of the baked product, and dough
CC properties e.g. a less soft dough, higher elasticity and lower
CC extensibility. The present amino acid sequence represents a Thermomyces
CC lanuginosus lipolytic enzyme variant of the invention.
CC Note: The present sequence is not shown in the specification but is
CC derived from the Thermomyces lanuginosus lipolytic enzyme (ABG32551)
CC sequence given on pages 20-21 of the specification.
XX
XX Sequence 269 AA;
XX
XX Query Match 24.1%; Score 360; DB 23; Length 269;
XX Best Local Similarity 31.7%; Pred. No. 4.9e-25;
XX Matches 90; Conservative 48; Mismatches 98; Indels 48; Gaps 10;
QY 27 ISEDLVSRVEMATISQAAYADL-----CNIPST-----IIRGEKIY-----NSQT 67
DB 2 VSQDLFNQNFPAQYSAAYCGKNNAPAGTNTCTGNACPEVEKADATFLYFSDSGVG 61
QY 68 DINGWILRDSKEIITVFRGSGDNTLQDNTYTLTPPDTLPQNGCEVHGYYIGWVS 127
DB 62 DVTGFLALDNTKLVLSFRGSRSIENWICNLFNLDLKEINDI--CSGCRGHGGFTSSWS 119
QY 128 VQDQVESLVKQVQSYQPDYALVTGHSGLASLAALTAQAQLSATYDNLRTYFGEPSGNQ 187
DB 120 VADTLRQKVEDAVREHPDYRVVFTGHSGLGALATVAGADLRGNGYDIDVPSYAPRVGNR 179
QY 188 AFASYMNDAFQASSPDTTQ----YFRVTHANDGIPNLPPVEQYAHGGVYVSWDPYS-- 241
DB 180 AFAEFL-----TVGTGGLYRITHNDIVRLPPREFGYSHPSPYWKSPGTPVP 229
QY 242 -AQTFTVCTGDEVQCEAGCGQGVNN-----AHTTYFGMTSGAC 279
DB 230 VTRNDIV-----KIEGIDATGNNQNPIDPITAHLLWTFGLI-GTC 268
RESULT 9
ID AAR22643
XX AAR22643 standard; Protein; 291 AA.
XX
XX AAR22643;
XX
XX 25-MAR-2003 (updated)
DT 06-OCT-1992 (first entry)
XX
XX Humicola lanuginosa lipase type III variant.
XX
XX Catalytic triad; trypsin; binding pocket; mutation; detergent; HLL.

OS Humicola lanuginosa.
XX Key Location/Qualifiers
FH Peptide 1..22
FT /note= "signal peptide of pre-pro-lipase"
FT Misc-difference 281
FT /label= Leu-> Thr.
FT /note= "indicated as position 259 in the patent"
XX
XX W09205249-A.
XX 02-APR-1992.
XX 12-SEP-1991; 91WO-US06605.
XX 13-SEP-1990; 90DK-0002194.
XX 13-SEP-1990; 90DK-0002195.
XX 13-SEP-1990; 90DK-0002196.
XX (NOVO) NOVO-NORDISK AS.
XX
XX Svendsen A, Clausen I, Packar SA, Gormsen E;
XX WPI; 1992-132120/16.
XX
XX Variant lipases with critical residues substd. or deleted -
XX confers different hydrophobicity or electrostatic properties on
XX binding pocket of enzyme contg. catalytic triad
XX
XX Claim 50; Page 51; 71pp; English.
XX
XX The sequence shows a lipase type III variant comprising a trypsin-like
XX catalytic triad including an active site serine located in a
XX predominantly hydrophobic, elongated binding pocket; and a surface
XX loop structure which covers the active site serine when the lipase is
XX in its inactive conformation and changes occur when the lipase is
XX activated to make the serine accessible to the lipid substrate, the
XX loop having a predominantly hydrophobic inner surface facing the
XX binding pocket and a primarily hydrophilic outer surface. The
XX variant is characterised by a substitution of Thr for Leu
XX in the loop structure (see feature table). The position of the
XX mutation given in the specification are assumed to use the
XX mature sequence of the lipase from Humicola lanuginosa strain
XX DSM 4106. However, the sequence given in the specification and
XX reproduced here is that of the pre-pro amino acid sequence of HLL
XX produced from the expression plasmid p960. Mutations were indicated
XX using this sequence as a base but discrepancies may occur between
XX residues stated in the patent and those indicated in the sequence.
XX The lipase variants have altered specificities and/or improved
XX properties, particularly w.r.t. accessibility of the active site
XX serine, and may be used as detergent additives.
XX See also AAR22629-45.
XX (Updated on 25-MAR-2003 to correct PA field.)
XX (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 291 AA;
XX
XX Query Match 24.1%; Score 359.5; DB 13; Length 291;
XX Best Local Similarity 31.8%; Pred. No. 6.1e-25;
XX Matches 95; Conservative 54; Mismatches 99; Indels 51; Gaps 12;
QY 14 VTAGHALAAS-TGISEDLYSRVEMATISQAAYADL-----CNIPST-----IIRG 59
DB 10 VSAWTAALASPIRREVSDQLFNQNFPAQYSAAYCGKNNAPAGTNTCTGNACPEVEKA 69
QY 60 EKLY-----NSQTDINGWILRDSKEIITVFRGSGDNTLQDNTYTLTPPDTLPQCN 113
DB 70 DATFLYFSDSGVGDVTGFLALDNTKLVLSFRGSRSIENWICNLFNLDLKEINDI--CS 127
QY 114 GCEVHGYYIGWVSQDQVESLVKQVQSYQPDYALVTGHSGLASLAALTAQAQLSATYDN 173
DB 128 GCRGHGGFTSSWSVADTLRQKVEDAVREHPDYRVVFTGHSGLGALATVAGADLRGNGYD 187

[illegible]

RESULT 10
ABG32566
ID ABG32566 standard; Protein; 269 AA.

CC further useful for preparing a baked product, e.g. pasta or noodles, as a
CC detergent additive and in leather industry. The invention is at least 4
CC plusCC more thermostable than the parent lipolytic enzyme. The addition
CC of the invention improves crumb structure of the baked product, and dough
CC properties e.g. a less soft dough, higher elasticity and lower
CC extensibility. The present amino acid sequence represents a Thermomyces
CC lanuginosus lipolytic enzyme variant of the invention.
CC Note: The present sequence is not shown in the specification but is
CC derived from the Thermomyces lanuginosus lipolytic enzyme (ABG32551)
CC sequence given on pages 20-21 of the specification.

RESULT 11

ABG32565
ID ABG32565 standard; Protein; 269 AA.

Query Match		23.9%; Score 356; DB 23; Length 269;
Best Local Similarity		31.8%; Pred. No. 1.2e-24;
Matches		90; Conservative 47; Mismatches 100; Indels 46; Gaps 10;
QY	27	ISEDYSLVEMWATISQAAAYADL-----CNIPST-----IIKGEKIY-----NSQT 67
Db	2	VSQDLNFQNLPAQYSAAYAAKGNRAPAGTITTCGNACPEVEKADATFLYSHFSDSGVG 61
QY	68	DINGWILRDDSSKEIITVPRGTSGDNLQDNTYLTLPDTPQNGCEVHGXYIGWVS 127
Db	62	DTVGTALDNTNKLIVLFRGSRSTENWTANLNFDLKEINDI--CSGCRGHGGFTSSWS 119
QY	128	VQDQVESLVKQVQSPYDVALVTGHSGLASLAALTAQLSATYDNIRLYTFGEPRSGNQ 187
Db	120	VADTLRQKVEDAVREHPDYRVFTGHSGLGALATVAGADLRNGYDIDVFSYGAPRVGNR 179
QY	198	APASVMNDAFOASSPDTTQ-----YFRVTHANDGIPNLPPVQGYANGGVYMSVDDPYSQA 243
Db	180	APAEPL-----TVQTGGLYRITHNTNDIVPLPRFRGYSHPSPEYWI--KSGT 226
QY	244	NTFVCTGP--EVOCCAGGQGVNN-----AHTYFGMTSGAC 279
Db	227	GVPTNRDIVKIGIDATGQNNQNPIDITAHLWYFGLI-GTC 268
RESULT 13		
ID	ABG32602	standard; Protein; 269 AA.
XX	AC	ABG32602;
XX	AC	
XX	DT	15-NOV-2002 (first entry)
XX	DE	Thermomyces lanuginosus lipolytic enzyme variant #50.
XX	KW	Fungal; lipolytic; enzyme; pitch trouble; mechanical pulp; paper-making;
XX	KW	dough; baked product; fabric; pasta; noodle; detergent additive; leather;
XX	KW	crumb structure; soft dough; elasticity; extensibility; variant.
XX	OS	Thermomyces lanuginosus.
Key	Location/Qualifiers	
FT	Misc-difference 27	/label= Asn, Arg, Ser
FT	Misc-difference 29	/note= "Pro substituted by Ser"
FT	Misc-difference 32	/note= "Thr substituted by Ser"
FT	Misc-difference 51	/label= Ile, Leu
FT	Misc-difference 76	/note= "Ile substituted by Val"
FT	Misc-difference 84	/note= "Arg substituted by Cys"
FT	Misc-difference 90	/label= Leu, Val
FT	Misc-difference 91	/label= Ala, Asn, Ser, Thr, Trp
FT	Misc-difference 93	/note= "Leu substituted by Phe"
FT	Misc-difference 94	/label= Lys, Arg, Ser
FT	Misc-difference 95	/note= "Phe substituted by Ile"
FT	Misc-difference 96	/label= Gly, Asn
FT	Misc-difference 101	/note= "Asn substituted by Asp"
FT	Misc-difference 111	/label= Arg, Gly
FT	Misc-difference 118	/note= "Arg substituted by Met"
FT	Misc-difference 131	
FT	Misc-difference 135	/note= "Ala substituted by Val"
FT	Misc-difference 137	/note= "His substituted by Tyr"
FT	Misc-difference 137	/note= "Asp substituted by Asn"
FT	Misc-difference 162	/note= "Asn substituted by Arg"
FT	Misc-difference 187	/note= "Val substituted by Ile"
FT	Misc-difference 211	/note= "Phe substituted by Tyr"
FT	Misc-difference 216	/note= "Ser substituted by Pro"
FT	Misc-difference 224	/label= Ile, Tyr
FT	Misc-difference 225	/note= "Gly substituted by Pro"
FT	Misc-difference 226	/note= "Thr substituted by Asn"
FT	Misc-difference 227	/label= Phe, Pro, Gly, Val, Xaa
FT	Misc-difference 228	/note= "Xaa is not further defined in the specification"
FT	Misc-difference 238	/label= Cys, Ile
FT	Misc-difference 238	/note= "Ile substituted by Val"
FT	Misc-difference 256	/note= "Pro substituted by Thr"
XX	XX	WO200255679-A2.
XX	XX	18-JUL-2002.
XX	XX	10-JAN-2002; 2002WO-DK000016.
XX	XX	10-JAN-2001; 2001DK-00000032.
XX	XX	18-JAN-2001; 2001US-262579P.
XX	XX	(NOVO) NOVOZYMES AS.
XX	XX	Minning S, Vind J, Glad SOS, Danielsen S, Borch K;
XX	XX	WPI; 2002-619105/66.
XX	XX	New variants of fungal lipolytic enzymes with improved thermostability
XX	XX	useful for hydrolysing a carboxylic ester, controlling pitch troubles
XX	XX	in mechanical pulp production or paper-making process and for preparing
XX	XX	dough -
XX	XX	Claim 20; Page -; 29pp; English.
XX	XX	The present invention relates to a new variant of a parent fungal
XX	XX	lipolytic enzyme. The invention comprises an amino acid sequence which
XX	XX	compared to the parent lipolytic enzyme comprises substitution of an
XX	XX	amino acid residue and which is more thermostable than the parent
XX	XX	lipolytic enzyme. The invention is useful for hydrolysing a carboxylic
XX	XX	acid ester, by incubating the ester with the lipase in the presence of
XX	XX	water, and for controlling pitch troubles in a process for the production
XX	XX	of mechanical pulp or a paper-making process using mechanical pulp. The
XX	XX	invention is also useful for preparing a dough or a baked product
XX	XX	prepared from the dough, and for hydrolysing, synthesising or
XX	XX	interesterifying as ester, by reacting the ester with water, reacting an
XX	XX	acid with an alcohol or interesterifying the ester with an acid, an
XX	XX	alcohol or a second ester in the presence of the invention, and also for
XX	XX	enzymatic removal of hydrophobic esters from fabrics. The invention is
XX	XX	further useful for preparing a baked product, e.g. pasta or noodles, as a
XX	XX	detergent additive and in leather industry. The invention is at least 4
XX	XX	plusC more thermostable than the parent lipolytic enzyme. The addition
XX	XX	of the invention improves crumb structure of the baked product, and dough
XX	XX	properties e.g. a less soft dough, higher elasticity and lower
XX	XX	extensibility. The present amino acid sequence represents a Thermomyces
XX	XX	lanuginosus lipolytic enzyme variant of the invention.
XX	XX	Note: The present sequence is not shown in the specification but is

CC derived from the Thermomyces lanuginosus lipolytic enzyme (ABG32551)
 CC sequence given on pages 20-21 of the specification.
 XX
 SQ Sequence 269 AA;
 Query Match 23.9%; Score 356; DB 23; Length 269;
 Best Local Similarity 31.3%; Pred. No. 1.2e-24;
 Matches 89; Conservative 48; Mismatches 99; Indels 48; Gaps 10;
 QY 27 ISEDLVSRVEMATISQAAYADLCNIPST-----IIKGE--KIYNSQF---- 67
 DB 2 VSODLFNQFNLFQAYSAAYCGKNYASAGSNITCTGNACPEVEKADATLYSPEDSGVG 61
 QY 68 DINGWILRDDSKKEITVFRGTGSDTNLQDWTYTLTPPTLPCQNGCEVHGYYLGWIS 127
 DB 62 DVTGFLADNTNKLVLSPRGSCSIENWXXFXILKEIDDI--CSGRGHXGFTSWMS 119
 QY 128 VDOVESLVKQVSYQVDPYALVTGHSLGASLAALTAQALSATVDNIRLTFGEPRSGNQ 187
 DB 120 VADTLRQKVEDVRETPNTRVFTGHSLGALATVAGADLRGRYDIDVFSYAPRVGNR 179
 QY 188 AFASYNDFAQASSPDTQ-----YFRVTHANDGIPNLPPVEQYAHGGVEYWSVDPYS-- 241
 DB 180 AFAEFL-----TIQTGGLYRITHNTDIVPRLPPREYGYSHPSPEYWIKNXPX 229
 QY 242 -AQNTFVCTGDEVOCCEAOGQGVNN-----AHTTYFGMTSGAC 279
 DB 230 VTRNDIV-----KVEGIDATGNNQNPIDITAHLWYFGLI-GTC 268
 RESULT 14
 AAR22640
 ID AAR22640 standard; Protein; 291 AA.
 AC AAR22640;
 XX
 DT 25-MAR-2003 (updated)
 DT 06-OCT-1992 (first entry)
 XX
 DE Humicola lanuginosa lipase type III variant.
 KW Catalytic triad; trypsin; binding pocket; mutation; detergent; HLL.
 XX
 OS Humicola lanuginosa.
 FH Key Location/Qualifiers
 FT Peptide 1..22
 FT Misc-difference 108 /note= "signal peptide of pre-pro-lipase"
 FT /label= Ile-> Thr.
 FT /note= "indicated as position 86 in the patent"
 XX
 PN W09205249-A.
 XX
 PD 02-APR-1992.
 XX
 PF 12-SEP-1991; 91WO-US06605.
 XX
 PR 13-SEP-1990; 90DK-0002194.
 PR 13-SEP-1990; 90DK-0002195.
 PR 13-SEP-1990; 90DK-0002196.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Svendsen A, Clausen I, Patkar SA, Gormsen B;
 XX
 DR WPI; 1992-132120/16.
 XX
 XX Variant lipases with critical residues substd. or deleted -
 PT confers different hydrophobicity or electrostatic properties on
 PT binding pocket of enzyme contg. catalytic triad
 XX
 PS Claim 50; Page 51; 7lpp; English.

XX The sequence shows a lipase type III variant comprising a trypsin-like
 CC catalytic triad including an active site serine located in a
 CC predominantly hydrophobic, elongated binding pocket; and a surface
 CC loop structure which covers the active site serine when the lipase is
 CC in its inactive conformation and changes occur when the lipase is
 CC activated to make the serine accessible to the lipid substrate, the
 CC loop having a predominantly hydrophobic inner surface facing the
 CC binding pocket and a primarily hydrophilic outer surface. The
 CC variant is characterised by a substitution of Thr for Ile
 CC in the loop structure (see feature table). The position of the
 CC mutation given in the specification are assumed to use the
 CC mature sequence of the lipase from Humicola lanuginosa strain
 CC DSM 4106. However, the sequence given in the specification and
 CC reproduced here is that of the pre-pro amino acid sequence of HLL
 CC produced from the expression plasmid p960. Mutations were indicated
 CC using this sequence as a base but discrepancies may occur between
 CC residues stated in the patent and those indicated in the sequence.
 CC The lipase variants have altered specificities and/or improved
 CC properties, particularly w.r.t. accessibility of the active site
 CC serine, and may be used as detergent additives.
 CC See also AAR22629-45.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 291 AA;
 Query Match 23.8%; Score 355.5; DB 13; Length 291;
 Best Local Similarity 31.4%; Pred. No. 1.4e-24;
 Matches 94; Conservative 54; Mismatches 100; Indels 51; Gaps 12;
 QY 14 VTAGHALAAS-TGISEDLYSRVEMATISQAAYADI-----CNIPST-----IIKG 59
 DB 10 VSAWALASPIRREVSQDLFNQFNLFQAYSAAYCGKNNDAPAGTNTCTGNACPEVEKA 69
 QY 60 EKIV-----NSQTDINGWILRDDSKKEITVFRGTGSDTNLQDWTYTLTPPTLPCN 113
 DB 70 DATFLVGFDSGVGDVGTGFLADNTNKLIVLSFRGSRSTENWGNLFDLKEINDI--CS 127
 QY 114 GCEVHGYYIGWVSQDVQVESLVKQVSYQVDPYALVTGHSLGASLAALTAQALSATVDN 173
 DB 128 GCRGHGDTSWRSVADTLRQKVEDAVREHPDYRVVFTGHSLGALATVAGADLRNGYD 187
 QY 174 IRLYTFGEPRSGNQAFASYNDFAQASSPDTQ-----YFRVTHANDGIPNLPPVEQYAH 229
 DB 188 IDVFSYCAPRVGNRAFAEFL-----TVQTGGLYRITHNTDIVPRLPPREFGYSH 237
 QY 230 GGVEYV-----SVDPYSAQNTFVCTGDEVOCCEAOGQGVNN-----AHTTYFGMTSGAC 279
 DB 238 SSPEYWIKSGTLVPVT-RNDIV-----KIEGIDATGNNQNPIDIPAHLWYFGLI-GTC 290
 RESULT 15
 AAR22641
 ID AAR22641 standard; Protein; 291 AA.
 XX
 AC AAR22641;
 XX
 DT 25-MAR-2003 (updated)
 DT 06-OCT-1992 (first entry)
 XX
 DE Humicola lanuginosa lipase type III variant.
 KW Catalytic triad; trypsin; binding pocket; mutation; detergent; HLL.
 XX
 OS Humicola lanuginosa.
 FH Key Location/Qualifiers
 FT Peptide 1..22
 FT Misc-difference 112 /note= "signal peptide of pre-pro-lipase"
 FT /label= Ile-> Thr.
 FT /note= "indicated as position 90 in the patent"

